

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,719
Source: PCT/10
Date Processed by STIC: 10/29/04

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/511,719

CRF Edit Date: 10/29/04
Edited by: h

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: invalid beginning/end-of-file text ; page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719

DATE: 10/29/2004
TIME: 18:25:42

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\10292004\J511719.raw

2 <110> APPLICANT: REGEN Biotech. Inc.
 4 <120> TITLE OF INVENTION: The method for measuring the amount of B??-?? protein and diagnostic kit
 5 using the same
 W--> 6 <130> FILE REFERENCE: 2fpo-10-14
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/511,719
 C--> 8 <141> CURRENT FILING DATE: 2004-10-18
 8 <160> NUMBER OF SEQ ID NOS: 10
 10 <170> SOFTWARE: KopatentIn 1.71
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 683
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Homo sapiens
 17 <400> SEQUENCE: 1
 18 Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu
 19 1 5 10 15
 21 Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
 22 20 25 30
 24 Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
 25 35 40 45
 27 Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
 28 50 55 60
 30 Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
 31 65 70 75 80
 33 Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
 34 85 90 95
 36 Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
 37 100 105 110
 39 Val Gly Ser Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
 40 115 120 125
 42 Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
 43 130 135 140
 45 Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
 46 145 150 155 160
 48 Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
 49 165 170 175
 51 Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
 52 180 185 190
 54 Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
 55 195 200 205
 57 Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
 58 210 215 220
 60 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
 61 225 230 235 240

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```

63 Asn Asn Ile Gln Gln Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
64          245          250          255
66 Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
67          260          265          270
69 Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
70          275          280          285
72 Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
73          290          295          300
75 Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
76 305          310          315          320
78 Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
79          325          330          335
81 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
82          340          345          350
84 Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
85          355          360          365
87 Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
88          370          375          380
90 Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
91 385          390          395          400
93 Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
94          405          410          415
96 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
97          420          425          430
99 Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
100         435         440         445
102 Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Leu Arg
103         450         455         460
105 Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
106 465         470         475         480
108 Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
109         485         490         495
111 Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
112         500         505         510
114 Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
115         515         520         525
117 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
118         530         535         540
120 Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
121 545         550         555         560
123 Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
124         565         570         575
126 Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
127         580         585         590
129 Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
130         595         600         605
132 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
133         610         615         620
135 Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln

```

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136	625	630	635	640
138	Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln			
139	645	650	655	
141	Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro			
142	660	665	670	
144	Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His			
145	675	680		
148	<210> SEQ ID NO: 2			
149	<211> LENGTH: 2691			
150	<212> TYPE: DNA			
151	<213> ORGANISM: Homo sapiens			
153	<400> SEQUENCE: 2			
154	gtttccccgt cggtcgctag ctgcgtcggt ggcgtcgct ccgcgtccatg ggcgtcttcg			60
156	tgcggctgtct ggctctcgcc ctggctctgg ccctggggcc cggcgcgacc ctggcggtgc			120
158	ccgccaagtc gcccattacag ctgggtctgc agcacagcag gctccggggc cgccagcagc			180
160	gccccaaacgt gtgtgtctgtc cagaaggta ttggactaa taggaagtac ttcaccaact			240
162	gcaaggcgtg gtaccaaagg aaaatctgtg gcaaatac acgtcatcagc tacgagtgt			300
164	gtcctggata tgaaaaggc cctggggaga agggctgtcc agcagcccta ccactctcaa			360
166	acctttacga gaccctggga gtcgttgat ccaccaccac tcagctgtac acggaccgca			420
168	cggagaagct gaggcctgag atggaggggc cggcagctt caccatctt gcccctagca			480
170	accaggccctg ggcctccctg ccagctgaag tgctggactc cctggtcagc aatgtcaaca			540
172	tttagctgtct caatgccctc cgctaccata tgggtggcag ggcgtctgt actgtatgagc			600
174	tgaaacacgg catgaccctc acctctatgt accagaattc caacatccag atccaccact			660
176	atcctaattgg gattgttaact gtgaactgtg cccggcttctt gaaagccgac caccatgca			720
178	ccaaacgggggt ggtcacccctc atcgataagg tcatactccac catcaccaac aacatccagc			780
180	agatcattga gatcgaggac acctttgaga cccttcgggc tgctgtggct gcatcaggc			840
182	tcaacacgat gcttaaggta aacggccagt acacgctttt ggcccccggacc aatgaggcct			900
184	tcgagaagat cccttagtggacttggaaacc gtatcctgggg cgaccaggaa gccctggag			960
186	acctgctgaa caaccacatc ttgaagtca tagtgtgtgc tgaagccatc gttggggggc			1020
188	tgtctgtaga gaccctggag ggcacgacac tggaggtggg ctgcagcggg gacatgctca			1080
190	ctatcaacgg gaaggcgatc atctccaata aagacatcct agccaccaac ggggtgtatcc			1140
192	actacattga tgagctactc atcccagact cagccaagac actatttggaa ttggctgcag			1200
194	agtctgtatgt gtccacagcc attgacctt tcagacaagg cggcctcggc aatcatctct			1260
196	ctggaaatgtg gcggttgacc ctccctggctc ccctgaatttgc tgtattcaaa gatggaaacc			1320
198	ctccaaatttgatg tggccatata aggaatttgc ttccggaaacca cataattaaa gaccagctgg			1380
200	cctctaaggta tctgttaccat ggacagaccc tggaaactct gggcggcaaa aaactgagag			1440
202	tttttgttta tcgtaatagc ctctgcattt agaacagctg catcgccggc cacgacaaga			1500
204	ggggggggta cgggaccctg ttcacgttgg accgggtgtc gaccccccata atggggactg			1560
206	tcatggatgt cctgaaaggta gacaatcgtt ttagcatgtc ggttagctgcc atccagtctg			1620
208	caggactgac ggagaccctc aaccgggaag gagtctacac agtctttgtc cccacaaatg			1680
210	aaggcattccg agccctgcca ccaagagaac ggagcagact cttggggat gccaaggaac			1740
212	ttgccaacat cctgaaatac cacattgggtt atgaaatcct ggttagcgga ggcacatgggg			1800
214	ccctgggtcg gctaaagtct ctccaaaggta acaagctggta agtcagcttggaaaacaatg			1860
216	tggtgatgtt caacaaggag cctgttgcgg agcctgacat catggccaca aatggcgtgg			1920
218	tccatgtcat caccaatgtt ctgcagccctc cagccaacag acctcaggaa agagggatg			1980
220	aacttgcaga ctctgcgtt gagatcttca aacaagcatc agcgttttcc agggcttccc			2040
222	agaggtctgt gcgactagcc cctgtctatc aaaagttatt agagaggatg aagcattagc			2100
224	ttgaaggact acaggagggaa tgcaccacgg cagctctccg ccaatttctc tcaagatttcc			2160
226	acagagactg tttgaatgtt ttcaaaaccca agtatcacac ttaatgtac atggccgcga			2220

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Input Set : A:\PTO.AMC.txt
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228	ccataatgag	atgtgaggcct	tgtgcatgtg	ggggaggagg	gagagagatg	tacttttaa	2280										
230	atcatgttc	ccctaaacat	ggctgttaac	ccactgcatg	cagaaacttg	gatgtca	2340										
232	cctgacattc	acttccagag	aggacctatc	ccaaatgtgg	aattgactgc	ctatgccaag	2400										
234	tccctggaaa	aggagcttca	gtattgtgg	gctcataaaa	catgaatcaa	gcaatccagc	2460										
236	ctcatggaa	gtcctggcac	agttttgtta	aagcccttgc	acagctggag	aatggcatc	2520										
238	attataagct	atgagttgaa	atgttctgtc	aatgtgtct	cacatctaca	cgtggcttgg	2580										
240	aggctttat	ggggccctgt	ccaggttagaa	aagaaatggt	atgtagagct	tagatttccc	2640										
242	tattgtgaca	gagccatggt	gtgttgtaa	taataaaacc	aaagaaacat	a	2691										
245	<210> SEQ ID NO: 3																
246	<211> LENGTH: 585																
247	<212> TYPE: PRT																
248	<213> ORGANISM: Homo sapiens																
250	<220> FEATURE:																
251	<221> NAME/KEY: PEPTIDE																
252	<222> LOCATION: (1)..(585)																
253	<223> OTHER INFORMATION: 69 to 653 amino acid sequence of human ID No.1																
256	<400> SEQUENCE: 3																
257	Tyr	Gln	Arg	Lys	Ile	Cys	Gly	Lys	Ser	Thr	Val	Ile	Ser	Tyr	Glu	Cys	
258	1			5				10				15					
260	Cys	Pro	Gly	Tyr	Glu	Lys	Val	Pro	Gly	Glu	Lys	Gly	Cys	Pro	Ala	Ala	
261				20				25				30					
263	Leu	Pro	Leu	Ser	Asn	Leu	Tyr	Glu	Thr	Leu	Gly	Val	Val	Gly	Ser	Thr	
264				35				40				45					
266	Thr	Thr	Gln	Leu	Tyr	Thr	Asp	Arg	Thr	Glu	Lys	Leu	Arg	Pro	Glu	Met	
267				50				55				60					
269	Glu	Gly	Pro	Gly	Ser	Phe	Thr	Ile	Phe	Ala	Pro	Ser	Asn	Glu	Ala	Trp	
270	65				70				75							80	
272	Ala	Ser	Leu	Pro	Ala	Glu	Val	Leu	Asp	Ser	Leu	Val	Ser	Asn	Val	Asn	
273					85				90							95	
275	Ile	Glu	Leu	Leu	Asn	Ala	Leu	Arg	Tyr	His	Met	Val	Gly	Arg	Arg	Val	
276					100				105							110	
278	Leu	Thr	Asp	Glu	Leu	Lys	His	Gly	Met	Thr	Leu	Thr	Ser	Met	Tyr	Gln	
279					115			120				125					
281	Asn	Ser	Asn	Ile	Gln	Ile	His	His	Tyr	Pro	Asn	Gly	Ile	Val	Thr	Val	
282					130			135				140					
284	Asn	Cys	Ala	Arg	Leu	Leu	Lys	Ala	Asp	His	His	Ala	Thr	Asn	Gly	Val	
285	145				150				155							160	
287	Val	His	Leu	Ile	Asp	Lys	Val	Ile	Ser	Thr	Ile	Thr	Asn	Ile	Gln		
288					165				170							175	
290	Gln	Ile	Ile	Glu	Ile	Glu	Asp	Thr	Phe	Glu	Thr	Leu	Arg	Ala	Ala	Val	
291					180			185				190					
293	Ala	Ala	Ser	Gly	Leu	Asn	Thr	Met	Leu	Glu	Gly	Asn	Gly	Gln	Tyr	Thr	
294					195			200				205					
296	Leu	Leu	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Ile	Pro	Ser	Glu	Thr	
297					210			215				220					
299	Leu	Asn	Arg	Ile	Leu	Gly	Asp	Pro	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Asn	
300	225				225			230				235				240	
302	Asn	His	Ile	Leu	Lys	Ser	Ala	Met	Cys	Ala	Glu	Ala	Ile	Val	Ala	Gly	
303					245			250				255					

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10292004\J511719.raw

305 Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser
 306 260 265 270
 308 Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp
 309 275 280 285
 311 Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile
 312 290 295 300
 314 Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val
 315 305 310 315 320
 317 Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu
 318 325 330 335
 320 Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe
 321 340 345 350
 323 Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg
 324 355 360 365
 326 Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly
 327 370 375 380
 329 Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr
 330 385 390 395 400
 332 Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys
 333 405 410 415
 335 Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro
 336 420 425 430
 338 Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser
 339 435 440 445
 341 Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn
 342 450 455 460
 344 Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg
 345 465 470 475 480
 347 Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu
 348 485 490 495
 350 Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser
 351 500 505 510
 353 Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys
 354 515 520 525
 356 Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro
 357 530 535 540
 359 Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile
 360 545 550 555 560
 362 Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp
 363 565 570 575
 365 Glu Leu Ala Asp Ser Ala Leu Glu Ile
 366 580 585
 369 <210> SEQ ID NO: 4
 370 <211> LENGTH: 1857
 371 <212> TYPE: DNA
 372 <213> ORGANISM: Mouse Intracisternal A-particle
 374 <400> SEQUENCE: 4
 375 gcaggtcccc ccaagtacc ctaccagctg gtgctgcagc atagccggct ccggggtcgc 60
 377 cagcacggcc ccaatgtatg tgctgtcgag aaggcattt gacccaacaa gaaatacttc 120

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/29/2004
PATENT APPLICATION: US/10/511,719 TIME: 18:25:44

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\10292004\J511719.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,719

DATE: 10/29/2004

TIME: 18:25:44

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10292004\J511719.raw

L:6 M:283 W: Missing Blank Line separator, <130> field identifier

L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date